

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: De Robertis, Edward M.
Bouwmeester, Tewis
- (ii) TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
Factors
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Majestic, Parsons, Siebert & Hsue
(B) STREET: Four Embarcadero Center, Suite 1100
(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: U.S.A.
(F) ZIP: 94111-4106
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Patent in Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/878,474
(B) FILING DATE: 18-JUN-1997
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/020,150
(B) FILING DATE: 20-JUN-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Siebert, J. Suzanne
(B) REGISTRATION NUMBER: 28,758
(C) REFERENCE/DOCKET NUMBER: 3100.002US1
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 415/248-5500
(B) TELEFAX: 415/362-5418

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Leu Leu Asn Val Leu Arg Ile Cys Ile Ile Val Cys Leu Val Asn
1 5 10 15
Asp Gly Ala Gly Lys His Ser Glu Gly Arg Glu Arg Thr Lys Thr Tyr
20 25 30
Ser Leu Asn Ser Arg Gly Tyr Phe Arg Lys Glu Arg Gly Ala Arg Arg
35 40 45
Ser Lys Ile Leu Leu Val Asn Thr Lys Gly Leu Asp Glu Pro His Ile
50 55 60
Gly His Gly Asp Phe Gly Leu Val Ala Glu Leu Phe Asp Ser Thr Arg
65 70 75 80
Thr His Thr Asn Arg Lys Glu Pro Asp Met Asn Lys Val Lys Leu Phe
85 90 95
Ser Thr Val Ala His Gly Asn Lys Ser Ala Arg Arg Lys Ala Tyr Asn
100 105 110
Gly Ser Arg Arg Asn Ile Phe Ser Arg Arg Ser Phe Asp Lys Arg Asn
115 120 125
Thr Glu Val Thr Glu Lys Pro Gly Ala Lys Met Phe Trp Asn Asn Phe
130 135 140
Leu Val Lys Met Asn Gly Ala Pro Gln Asn Thr Ser His Gly Ser Lys
145 150 155 160
Ala Gln Glu Ile Met Lys Glu Ala Cys Lys Thr Leu Pro Phe Thr Gln
165 170 175
Asn Ile Val His Glu Asn Cys Asp Arg Met Val Ile Gln Asn Asn Leu
180 185 190
Cys Phe Gly Lys Cys Ile Ser Leu His Val Pro Asn Gln Gln Asp Arg
195 200 205
Arg Asn Thr Cys Ser His Cys Leu Pro Ser Lys Phe Thr Leu Asn His
210 215 220

Leu Thr Leu Asn Cys Thr Gly Ser Lys Asn Val Val Lys Val Val Met
 225 230 235 240
 Met Val Glu Glu Cys Thr Cys Glu Ala His Lys Ser Asn Phe His Gln
 245 250 255
 Thr Ala Gln Phe Asn Met Asp Thr Ser Thr Thr Leu His His
 260 265 270

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1411 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATTCCTAA AAGCGGCACA GTGCAGGAAC AGCAAGTCGC TCAGAAACAC TGCAGGGTCT 60
 AGATATCATA CAATGTTACT AAATGTACTC AGGATCTGTA TTATCGTCTG CCTTGTGAAT 120
 GATGGAGCAG GAAACACTC AGAAGGACGA GAAAGGACAA AAACATATTC ACTTAACAGC 180
 AGAGGTTACT TCAGAAAAGA AAGAGGAGCA CGTAGGAGCA AGATTCTGCT GGTGAATACT 240
 AAAGGTCTTG ATGAACCCCA CATTGGGCAT GGTGATTTTG GCTTAGTAGC TGAACTATTT 300
 GATTCCACCA GAACACATAC AAACAGAAAA GAGCCAGACA TGAACAAAGT CAAGCTTTTC 360
 TCAACAGTTG CCCATGGAAA CAAAAGTGCA AGAAGAAAAG CTTACAATGG TTCTAGAAGG 420
 AATATTTTTT CTCGCCGTTT TTTTGATAAA AGAAATACAG AGGTTACTGA AAAGCCTGGT 480
 GCCAAGATGT TCTGGAACAA TTTTTTGGTT AAAATGAATG GAGCCCCACA GAATACAAGC 540
 CATGGCAGTA AAGCACAGGA AATAATGAAA GAAGCTTGCA AAACCTTGCC CTTCACTCAG 600
 AATATTGTAC ATGAAACTG TGACAGGATG GTGATACAGA ACAATCTGTG CTTTGGTAAA 660
 TGCATCTCTC TCCATGTTCC AAATCAGCAA GATCGACGAA ATACTTGTTT CCATTGCTTG 720
 CCGTCCAAAT TTACCCTGAA CCACCTGACG CTGAATTGTA CTGGATCTAA GAATGTAGTA 780
 AAGGTTGTCA TGATGGTAGA GGAATGCACG TGTGAAGCTC ATAAGAGCAA CTCCACCAA 840

ACTGCACAGT TTAACATGGA TACATCTACT ACCCTGCACC ATTAAAAGGA CTGTCTGCCA 900
TACAGTATGG AAATGCCCAT TTGTTGGAAT ATTCGTTACA TGCTATGTAT CTAAAGCATT 960
ATGTTGCCTT CTGTTTCATA TAACCACATG GAATAAGGAT TGTATGAATT ATAATTAACA 1020
AATGGCATT TGTGTAACAT GCAAGATCTC TGTTCCATCA GTTGCAAGAT AAAAGGCAAT 1080
ATTTGTTTGA CTTTTTCTA CAAAATGAAT ACCCAAATAT ATGATAAGAT AATGGGGTCA 1140
AAACTGTTAA GGGGTAATGT AATAATAGGG ACTAACAACC AATCAGCAGG TATGATTTAC 1200
TGGTCACCTG TTTAAAAGCA AACATCTTAT TGGTTGCTAT GGGTTACTGC TTCTGGGCAA 1260
AATGTGTGCC TCATAGGGGG GTTAGTGTGT TGTGTAAGTA ATTAATTGTA TTTATTTTCAT 1320
TGTTACAATG AAGAGGATGT CTATGTTTAT TTCACTTTTA TTAATGTACA ATAAATGTTC 1380
TTGTTTCTTT AAAAAAAAAA AAAAAGCTCGA G 1411

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ser Arg Thr Arg Lys Val Asp Ser Leu Leu Leu Leu Ala Ile Pro
1 5 10 15
Gly Leu Ala Leu Leu Leu Leu Pro Asn Ala Tyr Cys Ala Ser Cys Glu
20 25 30
Pro Val Arg Ile Pro Met Cys Lys Ser Met Pro Trp Asn Met Thr Lys
35 40 45
Met Pro Asn His Leu His His Ser Thr Gln Ala Asn Ala Ile Leu Ala
50 55 60
Ile Glu Gln Phe Glu Gly Leu Leu Thr Thr Glu Cys Ser Gln Asp Leu
65 70 75 80
Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys Thr Ile Asp Phe
85 90 95

Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys Glu Arg Ala Arg
 100 105 110
 Ala Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His Thr Trp Pro Glu
 115 120 125
 Ser Leu Ala Cys Glu Glu Leu Pro Val Tyr Asp Arg Gly Val Cys Ile
 130 135 140
 Ser Pro Glu Ala Ile Val Thr Val Glu Gln Gly Thr Asp Ser Met Pro
 145 150 155 160
 Asp Phe Ser Met Asp Ser Asn Asn Gly Asn Cys Gly Ser Gly Arg Glu
 165 170 175
 His Cys Lys Cys Lys Pro Met Lys Ala Thr Gln Lys Thr Tyr Leu Lys
 180 185 190
 Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Val Lys Val
 195 200 205
 Lys Cys His Asp Ala Thr Ala Ile Val Glu Val Lys Glu Ile Leu Lys
 210 215 220
 Ser Ser Leu Val Asn Ile Pro Lys Asp Thr Val Thr Leu Tyr Thr Asn
 225 230 235 240
 Ser Gly Cys Leu Cys Pro Gln Leu Val Ala Asn Glu Glu Tyr Ile Ile
 245 250 255
 Met Gly Tyr Glu Asp Lys Glu Arg Thr Arg Leu Leu Leu Val Glu Gly
 260 265 270
 Ser Leu Ala Glu Lys Trp Arg Asp Arg Leu Ala Lys Lys Val Lys Arg
 275 280 285
 Trp Asp Gln Lys Leu Arg Arg Pro Arg Lys Ser Lys Asp Pro Val Ala
 290 295 300
 Pro Ile Pro Asn Lys Asn Ser Asn Ser Arg Gln Ala Arg Ser
 305 310 315

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1875 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCCTT TCACACAGGA CTCCTGGCAG AGGTGAATGG TTAGCCCTAT GGATTGTT 60
TGTTGATTTT GACACATGAT TGATTGCTTT CAGATAGGAT TGAAGGACTT GGATTTTAT 120
CTAATTCTGC ACTTTTAAAT TATCTGAGTA ATTGTCATT TTGTATTGGA TGGGACTAAA 180
GATAAACTTA ACTCCTTGCT TTTGACTTGC CCATAAACTA TAAGGTGGGG TGAGTTGTAG 240
TTGCTTTTAC ATGTGCCCAG ATTTTCCCTG TATTCCCTGT ATTCCCTCTA AAGTAAGCCT 300
ACACATACAG GTTGGGCAGA ATAACAATGT CTCGAACAAG GAAAGTGGAC TCATTACTGC 360
TACTGGCCAT ACCTGGACTG GCGCTTCTCT TATTACCCAA TGCTTACTGT GCTTCGTGTG 420
AGCCTGTGCG GATCCCCATG TGCAAATCTA TGCCATGGAA CATGACCAAG ATGCCCAACC 480
ATCTCCACCA CAGCACTCAA GCCAATGCCA TCCTGGCAAT TGAACAGTTT GAAGGTTTGC 540
TGACCACTGA ATGTAGCCAG GACCTTTTGT TCTTTCTGTG TGCCATGTAT GCCCCATTT 600
GTACCATCGA TTTCCAGCAT GAACCAATTA AGCCTTGCAA GTCCGTGTGC GAAAGGGCCA 660
GGGCCGGCTG TGAGCCCATT CTCATAAAGT ACCGGCACAC TTGGCCAGAG AGCCTGGCAT 720
GTGAAGAGCT GCCCGTATAT GACAGAGGAG TCTGCATCTC CCCAGAGGCT ATCGTCACAG 780
TGGAACAAGG AACAGATTCA ATGCCAGACT TCTCCATGGA TTCAAACAAT GGAAATTGCG 840
GAAGCGGCAG GGAGCACTGT AAATGCAAGC CCATGAAGGC AACCCTAAAAG ACGTATCTCA 900
AGAATAATTA CAATTATGTA ATCAGAGCAA AAGTGAAAGA GGTGAAAGTG AAATGCCACG 960
ACGCAACAGC AATTGTGGAA GTAAAGGAGA TTCTCAAGTC TTCCCTAGTG AACATTCTTA 1020
AAGACACAGT GACACTGTAC ACCAACTCAG GCTGCTTG TG CCCCAGCTT GTTGCCAATG 1080
AGGAATACAT AATTATGGGC TATGAAGACA AAGAGCGTAC CAGGCTTCTA CTAGTGGAAG 1140
GATCCTTGGC CGAAAAATGG AGAGATCGTC TTGCTAAGAA AGTCAAGCGC TGGGATCAAA 1200
AGCTTCGACG TCCCAGGAAA AGCAAAGACC CCGTGGCTCC AATCCCAAC AAAACAGCA 1260
ATTCCAGACA AGCGCGTAGT TAGACTAACG GAAAGGTGTA TGGAACTCT ATGGACTTTG 1320
AAACTAAGAT TTGCATTGTT GGAAGAGCAA AAAAGAAATT GCACTACAGC ACGTTATATT 1380
CTATTGTTTA CTACAAGAAG CTGGTTTAGT TGATTGTAGT TCTCCTTTCC TTCTTTTTTT 1440

TTATAACTAT ATTTGCACGT GTTCCCAGGC AATTGTTTTA TTCAACTTCC AGTGACAGAG 1500
 CAGTGACTGA ATGTCTCAGC CTAAAGAAGC TCAATTCATT TCTGATCAAC TAATGGTGAC 1560
 AAGTGTTTGA TACTTGGGGA AAGTGAAC TAATGCAATGG TAAATCAGAG AAAAGTTGAC 1620
 CAATGTTGCT TTTCTGTAG ATGAACAAGT GAGAGATCAC ATTTAAATGA TGATCACTTT 1680
 CCATTTAATA CTTTCAGCAG TTTTAGTTAG ATGACATGTA GGATGCACCT AAATCTAAAT 1740
 ATTTTATCAT AAATGAAGAG CTGGTTTGA CTGTATGGTC ACTGTTGGGA AGGTAAATGC 1800
 CTACTTTGTC AATTCTGTTT TAAAATTGC CTAAATAAAT ATTAAGTCCT AAATAAAAAA 1860
 AAAAAAAAAA AAAAA 1875

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 979 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Leu Leu Leu Phe Arg Ala Ile Pro Met Leu Leu Leu Gly Leu Met
 1 5 10 15
 Val Leu Gln Thr Asp Cys Glu Ile Ala Gln Tyr Tyr Ile Asp Glu Glu
 20 25 30
 Glu Pro Pro Gly Thr Val Ile Ala Val Leu Ser Gln His Ser Ile Phe
 35 40 45
 Asn Thr Thr Asp Ile Pro Ala Thr Asn Phe Arg Leu Met Lys Gln Phe
 50 55 60
 Asn Asn Ser Leu Ile Gly Val Arg Glu Ser Asp Gly Gln Leu Ser Ile
 65 70 75 80
 Met Glu Arg Ile Asp Arg Glu Gln Ile Cys Arg Gln Ser Leu His Cys
 85 90 95
 Asn Leu Ala Leu Asp Val Val Ser Phe Ser Lys Gly His Phe Lys Leu
 100 105 110

Leu Asn Val Lys Val Glu Val Arg Asp Ile Asn Asp His Ser Pro His
 115 120 125
 Phe Pro Ser Glu Ile Met His Val Glu Val Ser Glu Ser Ser Ser Val
 130 135 140
 Gly Thr Arg Ile Pro Leu Glu Ile Ala Ile Asp Glu Asp Val Gly Ser
 145 150 155 160
 Asn Ser Ile Gln Asn Phe Gln Ile Ser Asn Asn Ser His Phe Ser Ile
 165 170 175
 Asp Val Leu Thr Arg Ala Asp Gly Val Lys Tyr Ala Asp Leu Val Leu
 180 185 190
 Met Arg Glu Leu Asp Arg Glu Ile Gln Pro Thr Tyr Ile Met Glu Leu
 195 200 205
 Leu Ala Met Asp Gly Gly Val Pro Ser Leu Ser Gly Thr Ala Val Val
 210 215 220
 Asn Ile Arg Val Leu Asp Phe Asn Asp Asn Ser Pro Val Phe Glu Arg
 225 230 235 240
 Ser Thr Ile Ala Val Asp Leu Val Glu Asp Ala Pro Leu Gly Tyr Leu
 245 250 255
 Leu Leu Glu Leu His Ala Thr Asp Asp Asp Glu Gly Val Asn Gly Glu
 260 265 270
 Ile Val Tyr Gly Phe Ser Thr Leu Ala Ser Gln Glu Val Arg Gln Leu
 275 280 285
 Phe Lys Ile Asn Ser Arg Thr Gly Ser Val Thr Leu Glu Gly Gln Val
 290 295 300
 Asp Phe Glu Thr Lys Gln Thr Tyr Glu Phe Glu Val Gln Ala Gln Asp
 305 310 315 320
 Leu Gly Pro Asn Pro Leu Thr Ala Thr Cys Lys Val Thr Val His Ile
 325 330 335
 Leu Asp Val Asn Asp Asn Thr Pro Ala Ile Thr Ile Thr Pro Leu Thr
 340 345 350
 Thr Val Asn Ala Gly Val Ala Tyr Ile Pro Glu Thr Ala Thr Lys Glu
 355 360 365
 Asn Phe Ile Ala Leu Ile Ser Thr Thr Asp Arg Ala Ser Gly Ser Asn
 370 375 380

Gly Gln Val Arg Cys Thr Leu Tyr Gly His Glu His Phe Lys Leu Gln
 385 390 395 400
 Gln Ala Tyr Glu Asp Ser Tyr Met Ile Val Thr Thr Ser Thr Leu Asp
 405 410 415
 Arg Glu Asn Ile Ala Ala Tyr Ser Leu Thr Val Val Ala Glu Asp Leu
 420 425 430
 Gly Phe Pro Ser Leu Lys Thr Lys Lys Tyr Tyr Thr Val Lys Val Ser
 435 440 445
 Asp Glu Asn Asp Asn Ala Pro Val Phe Ser Lys Pro Gln Tyr Glu Ala
 450 455 460
 Ser Ile Leu Glu Asn Asn Ala Pro Gly Ser Tyr Ile Thr Thr Val Ile
 465 470 475 480
 Ala Arg Asp Ser Asp Ser Asp Gln Asn Gly Lys Val Asn Tyr Arg Leu
 485 490 495
 Val Asp Ala Lys Val Met Gly Gln Ser Leu Thr Thr Phe Val Ser Leu
 500 505 510
 Asp Ala Asp Ser Gly Val Leu Arg Ala Val Arg Ser Leu Asp Tyr Glu
 515 520 525
 Lys Leu Lys Gln Leu Asp Phe Glu Ile Glu Ala Ala Asp Asn Gly Ile
 530 535 540
 Pro Gln Leu Ser Thr Arg Val Gln Leu Asn Leu Arg Ile Val Asp Gln
 545 550 555 560
 Asn Asp Asn Cys Pro Val Ile Thr Asn Pro Leu Leu Asn Asn Gly Ser
 565 570 575
 Gly Glu Val Leu Leu Pro Ile Ser Ala Pro Gln Asn Tyr Leu Val Phe
 580 585 590
 Gln Leu Lys Ala Glu Asp Ser Asp Glu Gly His Asn Ser Gln Leu Phe
 595 600 605
 Tyr Thr Ile Leu Arg Asp Pro Ser Arg Leu Phe Ala Ile Asn Lys Glu
 610 615 620
 Ser Gly Glu Val Phe Leu Lys Lys Gln Leu Asn Ser Asp His Ser Glu
 625 630 635 640
 Asp Leu Ser Ile Val Val Ala Val Tyr Asp Leu Gly Arg Pro Ser Leu
 645 650 655

Ser Thr Asn Ala Thr Val Lys Phe Ile Leu Thr Asp Ser Phe Pro Ser
 660 665 670
 Asn Val Glu Val Val Ile Leu Gln Pro Ser Ala Glu Glu Gln His Gln
 675 680 685
 Ile Asp Met Ser Ile Ile Phe Ile Ala Val Leu Ala Gly Gly Cys Ala
 690 695 700
 Leu Leu Leu Leu Ala Ile Phe Phe Val Ala Cys Thr Cys Lys Lys Lys
 705 710 715 720
 Ala Gly Glu Phe Lys Gln Val Pro Glu Gln His Gly Thr Cys Asn Glu
 725 730 735
 Glu Arg Leu Leu Ser Thr Pro Ser Pro Gln Ser Val Ser Ser Ser Leu
 740 745 750
 Ser Gln Ser Glu Ser Cys Gln Leu Ser Ile Asn Thr Glu Ser Glu Asn
 755 760 765
 Cys Ser Val Ser Ser Asn Gln Glu Gln His Gln Gln Thr Gly Ile Lys
 770 775 780
 His Ser Ile Ser Val Pro Ser Tyr His Thr Ser Gly Trp His Leu Asp
 785 790 795 800
 Asn Cys Ala Met Ser Ile Ser Gly His Ser His Met Gly His Ile Ser
 805 810 815
 Thr Lys Asp Ser Gly Lys Gly Asp Ser Asp Phe Asn Asp Ser Asp Ser
 820 825 830
 Asp Thr Ser Gly Glu Ser Gln Lys Lys Ser Ile Glu Gln Pro Met Gln
 835 840 845
 Ala Gln Ala Ser Ala Gln Tyr Thr Asp Glu Ser Ala Gly Phe Arg His
 850 855 860
 Ala Asp Asn Tyr Phe Ser His Arg Ile Asn Lys Gly Pro Glu Asn Gly
 865 870 875 880
 Asn Cys Thr Leu Gln Tyr Glu Lys Gly Tyr Arg Leu Ser Tyr Ser Val
 885 890 895
 Ala Pro Ala His Tyr Asn Thr Tyr His Ala Arg Met Pro Asn Leu His
 900 905 910
 Ile Pro Asn His Thr Leu Arg Asp Pro Tyr Tyr His Ile Asn Asn Pro
 915 920 925

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Val Ala Asn Arg Met His Ala Glu Tyr Glu Arg Asp Leu Val Asn Arg
 930 935 940
 Ser Ala Thr Leu Ser Pro Gln Arg Ser Ser Ser Arg Tyr Gln Glu Phe
 945 950 955 960
 Asn Tyr Ser Pro Gln Ile Ser Arg Gln Leu His Pro Ser Glu Ile Ala
 965 970 975
 Thr Thr Phe

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3655 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTCCCAG AGATGAACTC CTTGAGATTG TTTTAAATGA CTGCAGGTCT GGAAGGATTC 60
 ACATTGCCAC ACTGTTTCTA GGCATGAAAA AACTGCAAGT TTCAACTTTG TTTTGGTGTC 120
 AACTTTGATT CTTCAAGATG CTGCTTCTCT TCAGAGCCAT TCCAATGCTG CTGTTGGGAC 180
 TGATGGTTTT ACAACAGAC TGTGAAATTG CCCAGTACTA CATAGATGAA GAAGAACCCC 240
 CTGGCACTGT AATTGCAGTG TTGTCACAAC ACTCCATATT TAACACTACA GATATACCTG 300
 CAACCAATTT CCGTCTAATG AAGCAATTTA ATAATTCCCT TATCGGAGTC CGTGAGAGTG 360
 ATGGGCAGCT GAGCATCATG GAGAGGATTG ACCGGGAGCA AATCTGCAGG CAGTCCCTTC 420
 ACTGCAACCT GGCTTTGGAT GTGGTCAGCT TTTCCAAAGG ACACTTCAAG CTTCTGAACG 480
 TGAAAGTGA GGTGAGAGAC ATTAATGACC ATAGCCCTCA CTTTCCCAGT GAAATAATGC 540
 ATGTGGAGGT GTCTGAAAGT TCCTCTGTGG GCACCAGGAT TCCTTTAGAA ATTGCAATAG 600
 ATGAAGATGT TGGGTCCAAC TCCATCCAGA ACTTTCAGAT CTCAAATAAT AGCCACTTCA 660
 GCATTGATGT GCTAACCAGA GCAGATGGGG TGAAATATGC AGATTTAGTC TTAATGAGAG 720
 AACTGGACAG GGAAATCCAG CCAACATACA TAATGGAGCT ACTAGCAATG GATGGGGGTG 780

TACCATCACT ATCTGGTACT GCAGTGGTTA ACATCCGAGT CCTGGACTTT AATGATAACA 840
 GCCCAGTGTT TGAGAGAAGC ACCATTGCTG TGGACCTAGT AGAGGATGCT CCTCTGGGAT 900
 ACCTTTTGTGTT GGAGTTACAT GCTACTGACG ATGATGAAGG AGTGAATGGA GAAATTGTTT 960
 ATGGATTGAG CACTTTGGCA TCTCAAGAGG TACGTCAGCT ATTTAAAATT AACTCCAGAA 1020
 CTGGCAGTGT TACTCTTGAA GGCCAAGTTG ATTTTGAGAC CAAGCAGACT TACGAATTTG 1080
 AGGTACAAGC CCAAGATTTG GGCCCCAACC CACTGACTGC TACTTGTAAG GTAAGTGTTC 1140
 ATATACTTGA TGTAATGAT AATACCCAG CCATCACTAT TACCCCTCTG ACTACTGTAA 1200
 ATGCAGGAGT TGCCTATATT CCAGAAACAG CCACAAAGGA GAACTTTATA GCTCTGATCA 1260
 GCACTACTGA CAGAGCCTCT GGATCTAATG GACAAGTTCG CTGTACTCTT TATGGACATG 1320
 AGCACTTTAA ACTACAGCAA GCTTATGAGG ACAGTTACAT GATAGTTACC ACCTCTACTT 1380
 TAGACAGGGA AAACATAGCA GCGTACTCTT TGACAGTAGT TGCAGAAGAC CTTGGCTTCC 1440
 CCTCATTGAA GACCAAAAAG TACTACACAG TCAAGGTTAG TGATGAGAAT GACAATGCAC 1500
 CTGTATTTTC TAAACCCAG TATGAAGCTT CTATTCTGGA AAATAATGCT CCAGGCTCTT 1560
 ATATACTAC AGTGATAGCC AGAGACTCTG ATAGTGATCA AAATGGCAAA GTAAATTACA 1620
 GACTTGTGGA TGCAAAAGTG ATGGGCCAGT CACTAACAAC ATTTGTTTCT CTTGATGCGG 1680
 ACTCTGGAGT ATTGAGAGCT GTTAGGTCTT TAGACTATGA AAACTTAAA CAACTGGATT 1740
 TTGAAATTGA AGCTGCAGAC AATGGGATCC CTCAACTCTC CACTCGCGTT CAACTAAATC 1800
 TCAGAATAGT TGATCAAAAT GATAATTGCC CTGTGATAAC TAATCCTCTT CTTAATAATG 1860
 GCTCGGGTGA AGTTCTGCTT CCCATCAGCG CTCCTCAAAA CTATTTAGTT TTCCAGCTCA 1920
 AAGCCGAGGA TTCAGATGAA GGGCACAAC CCCAGCTGTT CTATACCATA CTGAGAGATC 1980
 CAAGCAGATT GTTTGCCATT AACAAAGAAA GTGGTGAAGT GTTCCTGAAA AAACAATTAA 2040
 ACTCTGACCA TTCAGAGGAC TTGAGCATAG TAGTTGCAGT GTATGACTTG GGAAGACCTT 2100
 CATTATCCAC CAATGCTACA GTTAAATTCA TCCTCACCAG CTCTTTTCCT TCTAACGTTG 2160
 AAGTCGTTAT TTTGCAACCA TCTGCAGAAG AGCAGCACCA GATCGATATG TCCATTATAT 2220
 TCATTGCAGT GCTGGCTGGT GGTTGTGCTT TGCTACTTTT GGCCATCTTT TTTGTGGCCT 2280
 GTACTTGTA AAAGAAAGCT GGTGAATTTA AGCAGGTACC TGAACAACAT GGAACATGCA 2340

ATGAAGAACG CCTGTTAAGC ACCCCATCTC CCCAGTCGGT CTCTTCTTCT TTGTCTCAGT 2400
 CTGAGTCATG CCAACTCTCC ATCAATACTG AATCTGAGAA TTGCAGCGTG TCCTCTAACC 2460
 AAGAGCAGCA TCAGCAAACA GGCATAAAGC ACTCCATCTC TGTACCATCT TATCACACAT 2520
 CTGGTTGGCA CCTGGACAAT TGTGCAATGA GCATAAGTGG ACATTCTCAC ATGGGGCACA 2580
 TTAGTACAAA GGACAGTGGC AAAGGAGATA GTGACTTCAA TGACAGTGAC TCTGATACTA 2640
 GTGGAGAATC ACAAAGAAG AGCATTGAGC AGCCAATGCA GGCACAAGCC AGTGCTCAAT 2700
 ACACAGATGA ATCAGCAGGG TTCCGACATG CCGATAACTA TTTCAGCCAC CGAATCAACA 2760
 AGGGTCCAGA AAATGGGAAC TGCACATTGC AATATGAAAA GGGCTATAGA CTGTCTTACT 2820
 CTGTAGCTCC TGCTCATTAC AATACCTACC ATGCAAGAAT GCCTAACCTG CACATACCGA 2880
 ACCATACCCT TAGAGACCCT TATTACCATA TCAATAATCC TGTGCTAAT CGGATGCACG 2940
 CGGAATATGA AAGAGATTTA GTCAACAGAA GTGCAACGTT ATCTCCGCAG AGATCGTCTA 3000
 GCAGATACCA AGAATTCAAT TACAGTCCGC AGATATCAAG ACAGCTTCAT CCTTCAGAAA 3060
 TTGCTACAAC CTTTTAATCA TTAGGCATGC AAGTGAGAAT GCACAAAGGC AAGTGCTTTA 3120
 GCATGAAAGC TAAATATATG GAGTCTCCCC TTTCCCTCTG ATGGATGGGG GGAGACACAG 3180
 GACAGTGCAT AAATATACAG CTGCTTTCTA TTTGCATTTC ACTTGGAAT TTTTGTTTT 3240
 TTTTACATAT TTATTTTTCC TGAATTGAAT GTGACATTGT CCTGTCACCT AACTAGCAAT 3300
 TAAATCCACA GACCTACAGT CAAATATTTG AGGGCCCCTG AAACAGCACA TCAGTCAGGA 3360
 CCTAAAGTGG CCTTTTTACT TTTAGCAGCT CCTGGGCTG CCCTCTGTGT TAATCAGCCC 3420
 CTGGTCAAGT CCTGAGTAGG ATCATGGCGT TTTTATATGC ATCTCACCTA CTTTGGACGT 3480
 GATTTACACA TAATAGGAAA CGCTTGGTTT CAGTGAAGTC TGTGTTGTAT ATATTCTGTT 3540
 ATATACACGC ATTTTGTGTT TGTGTATATA TTTCAAGTCC ATTCAGATAT GTGTATATAG 3600
 TGCAGACCTT GTAAATTAAA TATTCTGATA CTTTTTCCTC AATAAATATT TAAAT 3655

(2) INFORMATION FOR SEQ ID NO:7:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 323 amino acids
 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Val Cys Cys Gly Pro Gly Arg Met Leu Leu Gly Trp Ala Gly Leu
1 5 10 15
Leu Val Leu Ala Ala Leu Cys Leu Leu Gln Val Pro Gly Ala Gln Ala
20 25 30
Ala Ala Cys Glu Pro Val Arg Ile Pro Leu Cys Lys Ser Leu Pro Trp
35 40 45
Asn Met Thr Lys Met Pro Asn His Leu His His Ser Thr Gln Ala Asn
50 55 60
Ala Ile Leu Ala Met Glu Gln Phe Glu Gly Leu Leu Gly Thr His Cys
65 70 75 80
Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys
85 90 95
Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys
100 105 110
Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His
115 120 125
Ser Trp Pro Glu Ser Leu Ala Cys Asp Glu Leu Pro Val Tyr Asp Arg
130 135 140
Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Asp Gly Ala Asp
145 150 155 160
Phe Pro Met Asp Ser Ser Thr Gly His Cys Arg Gly Ala Ser Ser Glu
165 170 175
Arg Cys Lys Cys Lys Pro Val Arg Ala Thr Gln Lys Thr Tyr Phe Arg
180 185 190
Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Val Lys Met
195 200 205
Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys Glu Ile Leu Lys
210 215 220
Ala Ser Leu Val Asn Ile Pro Arg Asp Thr Val Asn Leu Tyr Thr Thr
225 230 235 240

Ser Gly Cys Leu Cys Pro Pro Leu Thr Val Asn Glu Glu Tyr Val Ile
245 250 255
Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly
260 265 270
Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg
275 280 285
Trp Asp Met Lys Leu Arg His Leu Gly Leu Gly Lys Thr Asp Ala Ser
290 295 300
Asp Ser Thr Gln Asn Gln Lys Ser Gly Arg Asn Ser Asn Pro Arg Pro
305 310 315 320
Ala Arg Ser

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AAGCCTGGGA CCATGGTCTG CTGCGGCCCG GGACGGATGC TGCTAGGATG GGCCGGGTTG	60
CTAGTCCTGG CTGCTCTCTG CCTGCTCCAG GTGCCCCGAG CTCAGGCTGC AGCCTGTGAG	120
CCTGTCCGCA TCCCGCTGTG CAAGTCCCTT CCCTGGAACA TGACCAAGAT GCCCAACCAC	180
CTGCACCACA GCACCCAGGC TAACGCCATC CTGGCCATGG AACAGTTCGA AGGGCTGCTG	240
GGCACCCACT GCAGCCCGGA TCTTCTCTTC TTCCTCTGTG CAATGTACGC ACCCATTTGC	300
ACCATCGACT TCCAGCACGA GCCCATCAAG CCCTGCAAGT CTGTGTGTGA GCGCGCCCGA	360
CAGGGCTGCG AGCCCATTCT CATCAAGTAC CGCCACTCGT GGCCGGAAAG CTTGGCCTGC	420
GACGAGCTGC CGGTGTACGA CCGCGGCGTG TGCATCTCTC CTGAGGCCAT CGTCACCGCG	480
GACGGAGCGG ATTTTCCTAT GGATTCAAGT ACTGGACACT GCAGAGGGGC AAGCAGCGAA	540
CGTTGCAAAT GTAAGCCTGT CAGAGCTACA CAGAAGACCT ATTTCCGGAA CAATTACAAC	600

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TATGTCATCC GGGCTAAAGT TAAAGAGGTA AAGATGAAAT GTCATGATGT GACCGCCGTT	660
GTGGAAGTGA AGGAAATTCT AAAGGCATCA CTGGTAAACA TTCCAAGGGA CACCGTCAAT	720
CTTTATACCA CCTCTGGCTG CCTCTGTCCT CCACTTACTG TCAATGAGGA ATATGTCATC	780
ATGGGCTATG AAGACGAGGA ACGTTCAGG TTACTIONTGG TAGAAGGCTC TATAGCTGAG	840
AAGTGGAAGG ATCGGCTTGG TAAGAAAGTC AAGCGCTGGG ATATGAAACT CCGACACCTT	900
GGACTGGGTA AACTGATGC TAGCGATTCC ACTCAGAATC AGAAGTCTGG CAGGAACTCT	960
AATCCCCGGC CAGCACGCAG CTAAATCCTG AAATGTAAAA GGCCACACCC ACGGACTCCC	1020
TTCTAAGACT GCGCTGGTG GACTAACAAA GGAAAACCGC ACAGTTGTGC TCGTGACCGA	1080
TTGTTTACCG CAGACACCGC GTGGCTACCG AAGTTACTTC CGGTCCCCTT TCTCCTGCTT	1140
CTTAATGGCG TGGGGTTAGA TCCTTTAATA TGTTATATAT TCTGTTTCAT CAATCACGTG	1200
GGGACTGTTC TTTTGCAACC AGAATAGTAA ATTAAATATG TTGATGCTAA GGTTCCTGTA	1260
CTGGACTCCC TGGGTTTAAT TTGGTGTTCT GTACCCTGAT TGAGAATGCA ATGTTTCATG	1320
TAAAGAGAGA ATCCTGGTCA TATCTCAAGA ACTAGATATT GCTGTAAGAC AGCCTCTGCT	1380
GCTGCGCTTA TAGTCTTGTG TTTGTATGCC TTTGTCCATT TCCCTCATGC TGTGAAAGTT	1440
ATACATGTTT ATAAAGGTAG AACGGCATT TGAATCAGA CACTGCACAA GCAGAGTAGC	1500
CCAACACCAG GAAGCATTTA TGAGGAAACG CCACACAGCA TGACTIONTTT TCAAGATTGG	1560
CAGGCAGCAA AATAAATAGT GTTGGGAGCC AAGAAAAGAA TATTTTGCCT GGTTAAGGGG	1620
CACACTGGAA TCAGTAGCCC TTGAGCCATT AACAGCAGTG TTCTTCTGGC AAGTTTTTGA	1680
TTTGTTTATA AATGTATTCA CGAGCATTAG AGATGAACTT ATAACTAGAC ATCTGTTGTT	1740
ATCTCTATAG CTCTGCTTCC TTCTAAATCA AACCCATTGT TGGATGCTCC CTCTCCATTC	1800
ATAAATAAAT TTGGCTTGCT GTATTGGCCA GGAAAAGAAA GTATTAAAGT ATGCATGCAT	1860
GTGCACCAGG GTGTTATTTA ACAGAGGTAT GTACTIONCTAT AAAAGACTAT AATTTACAGG	1920
ACACGGAAAT GTGCACATTT GTTTACTTTT TTTCTTCCTT TTGCTTTGGG CTTGTGATTT	1980
TGGTTTTTGG TGTGTTTATG TCTGTATTTT GGGGGGTGGG TAGGTTTAAG CCATTGCACA	2040
TTCAAGTTGA ACTAGATTAG AGTAGACTAG GCTCATTGGC CTAGACATTA TGATTTGAAT	2100

TTGTGTTGTT TAATGCTCCA TCAAGATGTC TAATAAAAGG AATATGGTTG TCAACAGAGA 2160
 CGACAACAAC AACAAA 2176

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Val Cys Gly Ser Pro Gly Gly Met Leu Leu Leu Arg Ala Gly Leu
 1 5 10 15
 Leu Ala Leu Ala Ala Leu Cys Leu Leu Arg Val Pro Gly Ala Arg Ala
 20 25 30
 Ala Ala Cys Glu Pro Val Arg Ile Pro Leu Cys Lys Ser Leu Pro Trp
 35 40 45
 Asn Met Thr Lys Met Pro Asn His Leu His His Ser Thr Gln Ala Asn
 50 55 60
 Ala Ile Leu Ala Ile Glu Gln Phe Glu Gly Leu Leu Gly Thr His Cys
 65 70 75 80
 Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys
 85 90 95
 Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys
 100 105 110
 Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His
 115 120 125
 Ser Trp Pro Glu Asn Leu Ala Cys Glu Glu Leu Pro Val Tyr Asp Arg
 130 135 140
 Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Asp Gly Ala Asp
 145 150 155 160
 Phe Pro Met Asp Ser Ser Asn Gly Asn Cys Arg Gly Ala Ser Ser Glu
 165 170 175

Arg Cys Lys Cys Lys Pro Ile Arg Ala Thr Gln Lys Thr Tyr Phe Arg
 180 185 190
 Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Ile Lys Thr
 195 200 205
 Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys Glu Ile Leu Lys
 210 215 220
 Ser Ser Leu Val Asn Ile Pro Arg Asp Thr Val Asn Leu Tyr Thr Ser
 225 230 235 240
 Ser Gly Cys Leu Cys Pro Pro Leu Asn Val Asn Glu Glu Tyr Ile Ile
 245 250 255
 Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly
 260 265 270
 Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg
 275 280 285
 Trp Asp Met Lys Leu Arg His Leu Gly Leu Ser Lys Ser Asp Ser Ser
 290 295 300
 Asn Ser Asp Ser Thr Gln Ser Gln Lys Ser Gly Arg Asn Ser Asn Pro
 305 310 315 320
 Arg Gln Ala Arg Asn
 325

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1893 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGCGGAGCGG GCCTTTTGGC GTCCACTGCG CGGCTGCACC CTGCCCCATC TGCCGGGATC	60
ATGGTCTGCG GCAGCCCGGG AGGGATGCTG CTGCTGCGGG CCGGGCTGCT TGCCCTGGCT	120
GCTCTCTGCC TGCTCCGGGT GCCCGGGGCT CGGGCTGCAG CCTGTGAGCC CGTCCGCATC	180
CCCCTGTGCA AGTCCCTGCC CTGGAACATG ACTAAGATGC CCAACCACCT GCACCACAGC	240

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ACTCAGGCCA ACGCCATCCT GGCCATCGAG CAGTTCGAAG GTCTGCTGGG CACCCACTGC	300
AGCCCCGATC TGCTCTTCTT CCTCTGTGCC ATGTACGCGC CCATCTGCAC CATTGACTTC	360
CAGCACGAGC CCATCAAGCC CTGTAAGTCT GTGTGCGAGC GGGCCCGGCA GGGCTGTGAG	420
CCCATACTCA TCAAGTACCG CCACTCGTGG CCGGAGAACC TGGCCTGCGA GGAGCTGCCA	480
GTGTACGACA GGGGCGTGTG CATCTCTCCC GAGGCCATCG TTA CTGCGGA CGGAGCTGAT	540
TTTCCTATGG ATTCTAGTAA CGGAACTGT AGAGGGGCAA GCAGTGAACG CTGTAAATGT	600
AAGCCTATTA GAGCTACACA GAAGACCTAT TTCCGGAACA ATTACAATA TGTCATTCGG	660
GCTAAAGTTA AAGAGATAAA GACTAAGTGC CATGATGTGA CTGCAGTAGT GGAGGTGAAG	720
GAGATTCTAA AGTCCTCTCT GGTAAACATT CCACGGGACA CTGTCAACCT CTATACCAGC	780
TCTGGCTGCC TCTGCCCTCC ACTTAATGTT AATGAGGAAT ATATCATCAT GGGCTATGAA	840
GATGAGGAAC GTTCCAGATT ACTCTTGGTG GAAGGCTCTA TAGCTGAGAA GTGGAAGGAT	900
CGACTCGGTA AAAAAGTTAA GCGCTGGGAT ATGAAGCTTC GTCATCTTGG ACTCAGTAA	960
AGTGATTCTA GCAATAGTGA TTCCACTCAG AGTCAGAAGT CTGGCAGGAA CTCGAACCCC	1020
CGGCAAGCAC GCAACTAAAT CCCGAAATAC AAAAAGTAAC ACAGTGGACT TCCTATTAAG	1080
ACTTACTTGC ATTGCTGGAC TAGCAAAGGA AAATTGCACT ATTGCACATC ATATTCTATT	1140
GTTTACTATA AAAATCATGT GATAACTGAT TATTACTTCT GTTTCTCTTT TGGTTTCTGC	1200
TTCTCTCTTC TCTCAACCCC TTTGTAATGG TTTGGGGGCA GACTCTTAAG TATATTGTGA	1260
GTTTTCTATT TCACTAATCA TGAGAAAAAC TGTTCTTTTG CAATAATAAT AAATTAAACA	1320
TGCTGTTACC AGAGCCTCTT TGCTGAGTCT CCAGATGTTA ATTTACTTTC TGCACCCCAA	1380
TTGGGAATGC AATATTGGAT GAAAAGAGAG GTTTCTGGTA TTCACAGAAA GCTAGATATG	1440
CCTTAAAACA TACTCTGCCG ATCTAATTAC AGCCTTATTT TTGTATGCCT TTTGGGCATT	1500
CTCCTCATGC TTAGAAAGTT CCAAATGTTT ATAAAGGTAA AATGGCAGTT TGAAGTCAAA	1560
TGTCACATAG GCAAAGCAAT CAAGCACCAG GAAGTGTTTA TGAGGAAACA ACACCCAAGA	1620
TGAATTATTT TTGAGACTGT CAGGAAGTAA AATAAATAGG AGCTTAAGAA AGAACATTTT	1680
GCCTGATTGA GAAGCACAAC TGAAACCAGT AGCCGCTGGG GTGTTAATGG TAGCATTCTT	1740
CTTTTGCAA TACATTTGAT TTGTTTATGA ATATATTAAT CAGCATTAGA GAAATGAATT	1800

ATAACTAGAC ATCTGCTGTT ATCACCATAG TTTTGTTTAA TTTGCTTCCT TTAAATAAA
CCCATTGGTG AAAGTCAAAA AAAAAAAAAA AAA

1860

1893

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